



## **RAW SEQUENCE LISTING ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 09/821,782A  
Source: OIPE  
Date Processed by STIC: 4/24/02

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202**
- 3. Hand Carry directly to:**  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
**Or**  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
- 4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202**

## Raw Sequence Listing Error Summary

O IPE

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> 09/821,782A
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) 215 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



OIPE

**Does Not Comply  
Corrected Diskette Needed**

**RAW SEQUENCE LISTING**  
PATENT APPLICATION: US/09/821,782A

DATE: 04/24/2002  
TIME: 14:09:40

Input Set : A:\821782seq.txt  
Output Set: N:\CRF3\04242002\I821782A.raw

4 <110> APPLICANT: Kumar Verma, Sunil  
5 Singh, Lalji  
7 <120> TITLE OF INVENTION: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION  
9 <130> FILE REFERENCE: U-013365-9  
11 <140> CURRENT APPLICATION NUMBER: 09/821782A  
C--> 13 <141> CURRENT FILING DATE: 2002-04-08  
15 <160> NUMBER OF SEQ ID NOS: 255

#### ERRORED SEQUENCES

4304 <210> SEQ ID NO: 215		
4306 <211> LENGTH: 22		
4308 <212> TYPE: DNA		
4310 <213> ORGANISM: Artificial Sequence		
W--> 4312 <220> FEATURE:	missing <220> Feature - required, see item 11 on error summary sheet	
4312 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b		
4313 gene of animal species in polymerase chain reaction		
OK<E--> 4315 <400> SEQUENCE: 215		
4318 atgcaaataag gaagtatcat tc	22	
4916 <210> SEQ ID NO: 244		
4918 <211> LENGTH: 472		
4920 <212> TYPE: DNA		
4922 <213> ORGANISM: Ovis vignei		
4924 <400> SEQUENCE: 244		
4926 taccatgagg acaaataatca ttctgaggag caacagttat taccaaccc tcattcagcaa	60	
4927 ttccatatat tggcacaaac ctatcgaaat gaatctgagg aggattctca gtagacaaag	120	
4928 ctaccctcac ccgattttc gccttcaact ttatccc attcatcatc gcagccctcg	180	
4929 ctatagttca cttactcttc ctccacgaaa caggatccaa taacccaca ggaattccat	240	
E--> 4930 cggacacaga caaaatcccc ttccnnnnnn nnnnnnnnat taaagacatt ctgggtgcca	300	
4931 tcctactaat cctcatcctc atgctgttag tactattcac gcctgactta ctggagacc	360	
4932 cagacaacta cacccagca aacccactta acactcccc tcacatcaaa cctgaatgat	420	
4933 atttcctatt tgcataatgca atcttacgat caatccctaa taaacttagga gg	472	
5112 <210> SEQ ID NO: 254		
5114 <211> LENGTH: 472		
5116 <212> TYPE: DNA		
5118 <213> ORGANISM: Cervus elaphus xanthopygus		
5120 <400> SEQUENCE: 254		
5122 taccatgagg acaaataatca ttctgaggag caacggcat taccaaccc ctctcagcaa	60	
5123 ttccatacat tggcacaaac ctatcgaaat ggatctgagg aggatctca gtagataaaag	120	
5124 caaccctaac ccgattttc gccttcaact ttatccc attatcatc gcagcactcg	180	
5125 ctatagttca cttactcttc ctccacgaga caggatccaa taacccaca ggaattccat	240	
5126 cagacgcaga caaaatcccc ttccatcctt actataccat taaagatatac tttaggcatt	300	

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/821,782A

DATE: 04/24/2002

TIME: 14:09:41

Input Set : A:\821782seq.txt

Output Set: N:\CRF3\04242002\I821782A.raw

5127 tacttctagt	actcttccta	atattactag	tattattcgc	accagacctg	cttggagacc	360
5128 cagacaacta	taccccgagca	aatccactca	acacacccccc	tcacataaa	cctgaatgat	420
5129 attcctatt	tgcatacgca	atcctacgat	cgattcccaa	caaacttagga	gg	472

E--> 5132 (1) -delete (non-ascii garbage)

VARIABLE LOCATION SUMMARY  
PATENT APPLICATION: US/09/821,782A

DATE: 04/24/2002  
TIME: 14:09:42

Input Set : A:\821782seq.txt  
Output Set: N:\CRF3\04242002\I821782A.raw

Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
in <220> to <223> section, please explain location of n or Xaa, and which  
residue n or Xaa represents.

Seq#:45; N Pos. 269,431  
Seq#:216; N Pos. 104,107,128,368,369,431  
Seq#:217; N Pos. 425,431  
Seq#:226; N Pos. 437  
Seq#:240; N Pos. 264,338  
Seq#:244; N Pos. 264,265,266,267,268,269,270,271,272,273,274,275,276,277  
Seq#:244; N Pos. 278

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/821,782A

DATE: 04/24/2002  
TIME: 14:09:42

Input Set : A:\821782seq.txt  
Output Set: N:\CRF3\04242002\I821782A.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:967 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45  
L:980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:240  
L:983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:420  
L:4312 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:215  
L:4315 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:215  
L:4331 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:216  
L:4340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:60  
L:4341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:120  
L:4345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:360  
L:4346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:420  
L:4358 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:217  
L:4373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217 after pos.:420  
L:4546 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:226  
L:4561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:226 after pos.:420  
L:4829 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:240  
L:4842 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:240 after pos.:240  
L:4843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:240 after pos.:300  
L:4909 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:243  
L:4930 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:244  
L:5132 M:254 E: No. of Bases conflict, this line has no nucleotides.